

Godbole, et al.

U.S. Application No. 09/756,247

**AMENDMENTS TO THE SPECIFICATION**

Please replace the existing paragraph beginning at page 12, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPITYVLQYLEKAGLLTEEIRSRVGFLEIGYQKELM  
YKHSNGSYSAFGERDGNNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS  
GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKDVDDPMVSQGLRCLKNSAT  
STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAISGESIYWSQKPTPSSNASPWSEPA  
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNA YGGFSSTQDTVVALQAL  
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of  $4.4e-87$ , protein database identification number entry = 1c3d [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 13, line 5, with the following rewritten paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSNMAIVEVKMLSGFSPM  
EGTNQLLLQQPLVKKVEFGTDTLNIYLDLIKNTQTYTFTISQSVLVTNLKPATIKVYDY  
YLPGSFKLSQYTTIVWSMNND

(designated as SEQ ID NO: 22) with PSI-BLAST e-value of  $4.4e-52$ , protein database identification number entry = 1bv8 [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 1349-1479 of SEQ ID NO: 4.--

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Please replace the existing paragraph beginning at page 134, line 12, with the following rewritten paragraph:

-- Complement component C3d homologous sequence

LQNLDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTEEIRSRAVGFLEIGYQKELM  
YKHSNGSYSAFGERDGNNGNTWLTAFTVKCFGQAQKFIFIDPKNIQDALKWMAGNQLPS  
GCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLEMGKD VDDPMVSQGLRCLKNSAT  
STTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAUSGESIYWSQKPTPSSNASPWSEPA  
AVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLAKQHNA YGGFSSTQDTVVALQAL  
AKYATTAY

(designated as SEQ ID NO: 21) with PSI-BLAST e-value of 4.4e-87, protein database identification number entry = 1c3d [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 977-1276 of SEQ ID NO: 4.--

Please replace the existing paragraph beginning at page 135, line 8, with the following rewritten paragraph:

--Receptor domain alpha-2-macroglobulin domain

NMKTFSLSVEIGKARCEQPTSPRSLTLTIHTSYVGSRSSSNMAIVEVKMLSGFSPM  
EGTNQLLLQQPLVKKVEFGTDTLNTYLDELIKNTQTYTFTISQSVLVTNLKPATIKVYDY  
YLPGSFKLSQYTIVWSMNDS

(designated as SEQ ID NO: 22) with PSI-BLAST e-value of 4.4e-52, protein database identification number entry = 1bv8 [Research collaboratory for Structural Bioinformatics. Berman et al., *Nucl. Acids Res.* 28:235-242 (2000)], verify score = 0.49, located at residues 1349-1479 of SEQ ID NO: 4.--